User Manual for Dendroscope V2.7.4

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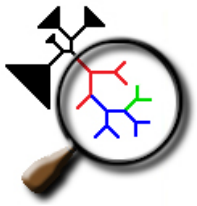

Dendroscope

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www-ab.informatik.uni-tuebingen.de/software/dendroscope

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1 Introduction

Disclaimer: This software is provided "AS IS" without warranty of any kind. This is developmental code, and we make no pretension as to it being bug-free and totally reliable. Use at your own risk. We will accept no liability for any damages incurred through the use of this software. Use of the Dendroscope is free, however the program is not open source.

Type-setting conventions: In this manual we use e.g. `Edit`→`Find` to indicate the `Find` menu item in the `Edit` menu.

How to cite: If you publish results obtained in part by using Dendroscope , then we require that you acknowledge this by `citing the program` as follows:

- Daniel H Huson, Daniel C Richter, Christian Rausch, Tobias Dezulian, Markus Franz and Regula Rupp. Dendroscope: An interactive viewer for large phylogenetic trees . BMC Bioinformatics 8:460, 2007, software freely available from www.dendroscope.org [4].

2 Program Overview

Dendroscope is a platform-independent software written in Java that enables conveniently to browse phylogenetic trees and networks with up to hundreds of thousands of taxa. Here is an overview of its features:

- There are 8 different tree views available, e.g. phylogram, cladogram or radial views.
- Its novel navigational features facilitate the analysis of large trees.
- It provides several tree manipulating functions like rerooting, subtree rotating, tree flipping and formating features like renaming, coloring or resizing edges, nodes and labels.
- A comprehensive set of export formats for the generation of images is available.
- User formated trees can be saved as a Dendroscope project file or as *.nexus*, or Newick tree files.
- Tree structures (single or multiple) can be loaded from *.tre* (Newick format) or *.nexus* files or entered manually.
- Rooted phylogenetic networks can be entered and visualized using the Extended Newick format [1].
- The program facilitates the computation of consensus trees and networks from a set of input trees.

3 Obtaining and Installing the Program

Dendroscope is written in Java and requires a Java runtime environment version 1.5 or later, freely available from www.java.org.

Dendroscope is installed using an installer program that is freely available from www.dendroscope.org. There are three different installers, targeting different operating systems:

- `Dendroscope_windows_2.7.4.exe` provides an installer for Windows.
- `Dendroscope_macos_2.7.4.dmg` provides an installer for MacOS.
- `Dendroscope_unix_2.7.4.sh` provides a shell installer for Linux and Unix.

Alternatively Dendroscope will be available as Java `Webstart application` from www-ab2.informatik.uni-tuebingen.de/webstart/dendroscope. If you need information concerning Java Webstart, go to http://java.sun.com/products/javawebstart/.

4 Getting Started

This section describes how to get started and to do the first steps of analyses using Dendroscope .

First, download an installer for the program from www.dendroscope.org, see Section 3 for details.

Start the program and load any *.tre*, *.nexus* or *.dendro* project file via `File→Open` . Alternatively, if the file was recently opened by the program, then it may be contained in the `File→Recent Files` submenu.
At startup, the tree will be scaled to fit to the window size.

Draw the tree differently by choosing one of the 8 provided views e.g. `Tree→Draw Rectangular Phylogram` , `Tree→Draw Rectangular Cladogram` , `Tree→Draw Slanted Cladogram` , `Tree→Draw Circular Phylogram` , `Tree→Draw Circular Cladogram` , `Tree→Draw Internal Circular Cladogram` , `Tree→Draw Radial Phylogram` , `Tree→Draw Radial Cladogram` . Try out the magnifier functions by clicking on `View→Use Magnifier` . Change any label font, size, color or edge/node size/width by opening the `Format Panel` via `Edit→Format` .

If you want to print the current image choose `File→Print` . In case you need a quality image of the tree, simply export it to several file formats via `File→Export Image` .

Finally, if you want to save the tree(s) and the formatting click `File→Save As` generating a *.dendro* project file. You can alos export the tree(s) by clicking `File→Export` . Choose one of the export formats (newick, nexus, dendro).

Note that only by saving a formatted tree as a *.dendro* project file you can save the formatting with the tree.

5 Main Window

The `Main` window is used to display the taxonomy and to control the program via the main menus.

We now discuss all menus of the `Main` window.

5.1 File Menu

The `File` menu contains the following file-related items:

- The `File→New` item opens an empty Dendroscope document.
- The `File→Open` item provides an `Open File` dialog to open one or more Dendroscope files (see Section 8) or *.tre* or *.nexus* files containing input data.
- The `File→Recent Files` item can be used to re-open a recently opened file.
- The `File→Save` item can be used to save the current tree and layout as Dendroscope project file.
- The `File→Save As` item can be used to save the current tree(s) as Dendroscope project file (.dendro) with the topology and layout.
- The `File→Export` item can be used to export the current tree(s) to Newick or Nexus file format. Note that only the topology but not the layout will be saved.
- The `File→Duplicate` item opens an additional window of Dendroscope containing the current tree.
- The `File→Export Image` item opens the `Export Image` dialog which is used to save the current tree in a number of different graphics formats, see Section 8.5.
- The `File→Print` item is used to print the current tree.
- The `File→Close` item closes the current window. In case only one window is opened, the application exits.
- The `File→Quit` item quits the program. Under `MacOS` , this item is contained in the Dendroscope menu.

5.2 Edit Menu

The `Edit` menu contains the usual edit-related items:

- The `Edit→Copy` item is used to copy the current tree or all selected trees.
- The `Edit→Paste` item is used to paste the copied trees to a new tab.
- The `Edit→Find/Replace` item opens the `Find` window which can be used to search for taxa and labels.
- The `Edit→Find Again` item finds the next occurrence of a search string.
- The `Edit→Reroot` item reroots the tree at the specified node or edge. If more than node is selected, all selected taxon labels are intepreted as *outgroup* taxa and the program determines the "tightest" rooting so that the outgroup appear together below the root.

- The `Edit→Swap Subtrees` item swaps the subtree (or subtrees) at the specified node (or nodes), see also Section 7.3
- The `Edit→Rotate Subtrees` item rotates the subtree(s) at the specified node(s).
- The `Edit→Reorder Subtrees` item opens a dialog that allows one to specific any type of reordering of the children of a node using "drag and drop".
- The `Edit→Delete Taxa` item removes the selected subtree form the current tree.
- The `Edit→Unlock Edge Lengths` item is used to "unlock edge lengths" so that the user is allowed to move individual nodes and internal edge points.
- The `Edit→Format` item opens a `Format Panel` which provides several possibilities to change color, fonts, node and edge shapes and the positioning of the labels of the tree.

5.3 Select Menu

The `Select` menu contains items for selecting different sets of substructures of the tree.

- The `Select→Select All` item is used to select all nodes, edges and labels.
- The `Select→Select Nodes` item is used to select all nodes.
- The `Select→Select Edges` item is used to select all edges.
- The `Select→From Previous Window` item is used to apply the selection of the previous window to the active window.
- The `Select→Deselect All` item is used to deselect all nodes, edges and labels that are currently selected.
- The `Select→Deselect Nodes` item is used to deselect all nodes that are currently selected.
- The `Select→Deselect Edges` item is used to deselect all edges that are currently selected.
- The `Select→Select Labeled Nodes` item is used to select all labeled nodes.
- The `Select→Select Leaves` item is used to select all leaves.
- The `Select→Select Subtree` item is used to select the subtree below a selected inner node.
- The `Select→Select Induced Tree` item is used to select a subtree induced by the set of currently selected nodes.
- The `Select→Select Spanned Edges` item is used to select all edges spanned by the set of currently selected nodes.
- The `Select→Select Root` item is used to select the root node of the tree.

- The `Select→Select Non-Terminal` item is used to select all non-terminal nodes and edges.
- The `Select→Select Special` item is used to select all edges leading to reticulation nodes in networks.
- The `Select→Invert Selection` item is used to invert the current selection.
- The `Select→Scroll to Selection` item is used to scroll to the current selection.
- The `Select→List Selected Taxa` item is used to list all selected taxa.

5.4 Options Menu

The `Options` menu contains items for collapsing nodes and extracting subtrees.

- The `Options→Collapse` item enables to collapse a subtree at a selected specified node. The former subtree is replaced by a new "edge" with label [...].
- The `Options→Uncollapse` item is used to uncollapse (expand) a selected, collapsed subtree.
- The `Options→Uncollapse Subtree` item is used to uncollapse (expand) all collapsed subtrees of a selected node.
- The `Options→Collapse Complement` item is used to collapse all subtrees except the currently selected part of the tree.
- The `Options→Collapse at Level` item is used to collapse all subtrees at the specified level from the root.
- The `Options→Extract Subtree` item is used to extract a selected subtree to a new file.
- The `Options→Load Taxon Images` item is used to specify a directory containing image files. Dendroscope tries to match taxon names to the names of images files and for each match found, Dendroscope shows the image near the node representing the given taxon.
- The `Options→Image Size` item is used to set the size of the image for the currently selected nodes.
- The `Options→Image Position` submenu is used to determine the relative positions of images in relative to the corresponding nodes (North, South, East, West, Radial).
- The `Options→Strict Consensus` item is used to compute the *strict consensus* of a set of trees.
- The `Options→Loose Consensus` item is used to compute the *loose consensus* of a set of trees.
- The `Options→Majority Consensus` item is used to compute the *majority consensus* of a set of trees.

- The `Options→LSA Consensus` item is used to compute the *LSA consensus* of a set of trees.
- The `Options→Network Consensus` item is used to compute a *rooted network consensus* of a set of trees. If the input set contains more than two trees, then the user can set a threshold that determines the percentage of input trees that a cluster must be contained in to make it into the output rooted network. The user can also decide whether the program should come a *cluster network* [6] that shows the clusters in a *hardwired representation* , a *galled network* [5] that represents the clusters in a topologically restricted *softwired representation* , or a *minimum network* that attemps to represent the clusters in a network of minimum *level* , as described in *Van Iersel et al, submitted, 2009.*
- The `Options→Network for Multi-Labeled Tree` menu item is used to compute a rooted phylogenetic network for a multi-labeled tree such that the network contains each label (or taxon) exactly once. There are three methods available here: the *Cluster method* extracts all the clusters in the tree and constructs a cluster network. The *exact method* computes the nested label for the root node of the tree and then constructs the corresponding network for that label, see Huber, Oxelman, Lott and Moulton (2006). The *LevelK* method extracts all clusters and then seeks to compute a level-k network of minimum level k for the clusters.

Note that Dendroscope does not require that the trees all contain exactly the same set of taxa to be able to compute a consensus (unlike most other programs).

5.5 Tree Menu

The `Tree` menu contains items for different tree and network views [3].

- The `Tree→Draw Rectangular Phylogram` item is used to draw the tree as rectangular phylogram.
- The `Tree→Draw Rectangular Cladogram` item is used to draw the tree as rectangular cladogram.
- The `Tree→Draw Slanted Cladogram` item is used to draw the tree as slanted cladogram.
- The `Tree→Draw Circular Phylogram` item is used to draw the tree as circular phylogram.
- The `Tree→Draw Circular Cladogram` item is used to draw the tree as circular cladogram.
- The `Tree→Draw Internal Circular Cladogram` item is used to draw the tree as circular cladogram with leaves on the inside.
- The `Tree→Draw Radial Phylogram` item is used to draw the tree as radial phylogram.
- The `Tree→Draw Radial Cladogram` item is used to draw the tree as radial cladogram.
- The `Tree→Previous Tree` item is used to switch to the last opened tree.
- The `Tree→Next Tree` item is used to switch to the next opened tree.

- The `Tree→Ladderize Left` item is used to order the tree so that the largest clades appear leftmost (uppermost in the view).
- The `Tree→Ladderize Right` item is used to order the tree so that the largest clades appear rightmost (lowermost in the view).
- The `Tree→Ladderize Random` item is used to order the clades randomly.

5.6 View Menu

The `Views` menu contains items for scaling the tree, using the magnifier and showing/hiding labels.

- The `View→Zoom to Fit` item is used to scale the tree to fit the window.
- The `View→Fully Contract` item is used to contract the tree.
- The `View→Fully Expand` item is used to expand the whole tree.
- The `View→Use Magnifier` item is used to turn the magnifier functionality on and off.
- The `View→Magnify All Mode` item modifiers the magnification process so that the whole tree gets mapped into the magnifier.
- The `View→Show Node Labels` item is used to make all node labels visible.
- The `View→Hide Node Labels` item is used to hide all node labels.
- The `View→Show Edge Weights` item is used to make edge weights visible.
- The `View→Show Edge Labels` item is used to make edge labels visible.
- The `View→Hide Edge Labels` item is used to hide edge labels.
- The `View→Sparse Labels` item instructs the program to show only a subset of the taxon labels, thus avoiding overlapping labels.
- The `View→Radial Labels` item instructs the program to rotate leaf labels to match the orientation of the edges that lead to them.
- The `View→Reposition Labels` item sets all the labels to their original position.

5.7 Window Menu

The `Window` menu contains a number of window-related commands as well as a list of all currently open windows.

- The `Window→About` item opens a splash screen showing the program version. In MacOS, this can be found under `Dendroscope→About` .

- The `Window→How to Cite` item shows the citation info for this software which is: Daniel H Huson, Daniel C Richter, Christian Rausch, Tobias Dezulian, Markus Franz and Regula Rupp. Dendroscope: An interactive viewer for large phylogenetic trees . BMC Bioinformatics 8:460, 2007.
- The `Window→Set Window Size` item is used to set the size of the `Main` window.
- The `Window→Command-line Syntax` item lists all commands supported by the program.
- The `Window→Execute Command` item opens a window that can be used to enter a command (see command).
- The `Window→Add Tree or Network` item opens a window to enter tree or network manually in Newick Format.
- The `Window→Message Window` item is used to open the `Message` window.
- If several program windows are openend, they are listed at the end of the window menu.

5.8 Toolbar

For easier access of frequently used functions, a *Toolbar* is provided with the following functions:

- `File→Open` , `File→Save As` , `File→Print` , `File→Export Image` , `Edit→Format`
- The `Expand view vertically` button expands the tree vertically.
- The `Contract view vertically` button shrinks the tree vertically.
- The `Expand view horizontally` button expands the tree horizontally.
- The `Contract view horizontally` button shrinks the tree horizontally.
- The `Rotate Left` button rotates the whole tree to the left.
- The `Rotate Right` button rotates the whole tree to the right.
- `View→Zoom to Fit` , `View→Fully Contract` , `View→Fully Expand` , `View→Use Magnifier` , `Tree→Draw Rectangular Phylogram` , `Tree→Draw Rectangular Cladogram` , `Tree→Draw Slanted Cladogram` , `Tree→Draw Circular Phylogram` , `Tree→Draw Circular Cladogram` , `Tree→Draw Internal Circular Cladogram` , `Tree→Draw Radial Phylogram` , `Tree→Draw Radial Cladogram` , `Edit→Find` , `Tree→Ladderize Left` , `Tree→Ladderize Right` , `Tree→Ladderize Random` `Tree→Ladderize Random` `Edit→Reroot` `Edit→Swap Subtree`

5.9 Context Menus

A right mouse click on a node opens a context menu which allows to edit the node label, open the `Format Panel`, show or hide node labels, copy the node label, select the subtree starting from this node, and swap the subtree starting from this node.

A right mouse click on an edge opens a context menu which allows to edit the edge label, open the `Format Panel`, show or hide edge labels, and copy the edge label.

A right mouse click beside the tree opens a context menu which allows to select or deselect all edges, nodes, and labels.

5.10 Side Bar

The *Side Bar* on the left contains a list of all trees in the current file. The arrows on top can be used to browse the list. Additionally, one can change the order of the list by dragging and dropping single trees to a new position in the list. The sidebar can be made (in)visible when clicking the small (left) right arrow located on the sidebar itself.

Right-clicking on one of the trees listed in the sidebar opens a popup menu with the following items:

- The `Copy` item can be used to copy a tree.
- The `Remove` item can be used to remove a tree for the list of trees.
- The `Rename` item can be used to rename a tree.
- The `Duplicate` item can be used to duplicate a tree.
- The `Clear Formatting` item can be used to clear all formating of a tree (such as choice of colors and fonts, etc.).

5.11 Consensus Bar

The *Consensus Bar* allows direct access to the following menu items:

- The `Options→Strict Consensus` item.
- The `Options→Loose Consensus` item.
- The `Options→Majority Consensus` item.
- The `Options→LSA Consensus` item.
- The `Options→Network Consensus` item.

5.12 Status Line

The `Status Line` at the bottom of the program window shows the index of the current tree, the total number of trees, the number of nodes and edges and the available space of the reserved memory.

6 Additional Windows

6.1 Format Panel

The `Format Panel` can be opened via `Edit→Format` or by a right mouse click after selecting elements of the tree like edges, nodes or labels. You can format them as follows:

- Edges can have their edge width and edge width set.
- Edges can be assigned three types of shapes: straight edges, curved edges and angular edges, the effect of which depends on the current view.
- Nodes can be assigned certain shapes: square nodes, circle nodes or none. Square and circle node shapes. They can have their node size and node color set.
- If a selected node or edge has a label, then you can choose its font family, font style or font size.
- Labels can be switched on and off, and can be rotated to the left or right. .

Configuration changes are applied immediately. The `Options→Save Font As Default` menu item can be used to set the default font, style and size used by the program. .

6.2 Find Window

The `Find` window can be opened using the `Edit→Find/Replace` item. Its purpose is to find and also to replace taxa labels in the tree. Enter a query specifying the name of a taxon in the top text region. Use the following check boxes to configure the search:

- If the `Match Whole` item is selected, then only taxa or labels matching the complete query string will be returned.
- If the `Respect Case` item is selected, then the case of letters is distinguished in comparisons.
- If the `Regular Expression` item is selected, the query is interpreted as a Java regular expression (see example further down).

If a searched label is "hidden" inside a bounding box (black opaque area of tree) or in a collapsed branch, it will be highlighted.

Press the `Close`, `Find First`, `Find Next` or `Find All` buttons to close the dialog, or find the first, or next occurrence of the query, respectively.

Alternatively, use the `From File` button to find all nodes that match any line of a given input file. The `Match Whole`, `Respect Case` and `Regular Expression` buttons apply to this type of search, too.

Regular Expressions are powerful and flexible text-processing tools. They allow to specify complex patterns of text that can be discovered in an input string.

Example 1:

Each of the following represent valid regular expressions, and all will successfully match the character sequence "`Escherichia`":

- Escherichia
- E.*
- [eE]scherichia
- [eE]sch[aeiou][a-z]ichi.*

Example 2:

To select the five taxa simutaneously, e.g. Human, Mouse, Dog, Cat and Rat, use the following expression: `Human|Mouse|Dog|cat|Rat` and then press `Find All` .

For an extensive list of metacharacters and futher explanations go to http://java.sun.com/j2se/1.5.0/docs/api/java/util/regex/Pattern.html

6.3 Message Window

The `Message` window is opened using the `Window→Message Window` item. The program writes all internal messages to this window. The window contains the usual File and Edit menu items.

6.4 Export Image Dialog

The `Export Image` dialog is opened using the `File→Export Image` item. This dialog is used to save an image of the current tree in a number of different formats, see Section 8.5.

The format is chosen from a menu. There are two radio buttons `Save whole image` to save the whole image, and `Save visible region` to save only the part of the image that is currently visible in the main viewer. If the chosen format is `EPS` , then selecting the `Convert text to graphics` check box will request the program to render all text as graphics, rather than fonts.

Pressing the apply button will open a standard file save dialog to determine where to save the graphics file.

6.5 About Window

The `About` Window is opened using the `Window→About` submenu (`Dendroscope→About` in MacOS). It reports the version of the program and its authors.

7 Additional Features

7.1 Using the Mouse to Select

Nodes, edges and labels can also be selected by clicking on them , shift-clicking to extend a selection or by (shift-) dragging the mouse to perform rubber-band selection in which all objects contained within a dragged rectangle are selected.

7.2 Magnifier Functionality

Dendroscope provides the user with a *magnifier functionality* that can be used to magnify portions of the tree.

Selecting the `View→Use Magnifier` item adds a magnifier layer to the view.

- *Magnifier band*: For all rooted views (rectangular and slanted view) a *magnifier band* is laid over the tree.
- *Magnifier disk*: For all unrooted views (radial and circular tree view) a *circular* magnifier is laid over the tree.

The magnifier can be pulled to a desired position by grabbing its frame with the mouse. The radius/width of the magnifier can be changed by dragging the rhomb at the magnifier's border line. The zoom factor of the magnifier can be changed via the [+,-] button.
Two magnifier modes are available depending on the current tree view:

7.3 Navigating trees with keys and mouse wheel

Dendroscope allows one to browse and analyze trees. `Navigating trees` is facilitated by some `key bindings` :

- *Scrolling:* Hold down the Shift button and use the mouse wheel to scroll top-down.
  Hold down the Alt and Shift buttons and use the mouse wheel to scroll right-left.
- *Zooming:* Use the mouse wheel to zoom the tree. Zooming is centered on the current mouse position. Alternatively, use the arrow keys to scroll the tree, or additionally press the shift key to zoom the graph in horizontal or vertical direction. Use the alt and control keys for acceleration.
- *Rotating:* For circular and radial drawings, use the shift-key and left and right arrow keys to rotate the tree.

8 File Formats

Dendroscope uses its own file format to store the data of the modified and/or formatted tree. By convention, we use the suffix `.dendro` for Dendroscope files.

8.1 Dendroscope Files

Dendroscope saves trees in a simple text-based format with the file extension `.dendro`. It contains the tree in Newick notation and additional (machine-readable) information on the view, selections, coloring etc. of the saved trees.

Trees can also be saved in Nexus and Newick format. However, when these formats are used, all information on the layout of the trees, fonts, colors, linewidths etc are lost.

8.2 Nexus files

Dendroscope can read a Nexus file that contains a Nexus trees block and can export trees in this format.

8.3 Newick files

Dendroscope can read Newick files and can export trees in this format.

8.4 Extended Newick format and rooted phylogenetic networks

The *Extended Newick* format was designed as an extension of the Newick format to be able to describe rooted phylogenetic networks in bracket notation. Unfortunately, there is not just one such format, but a number of different ones. Dendroscope implements a version of the Extended-Newick format that arose out of discussions that took place during the Phylogenetics Programme at the Isaac Newton Institute in 2007.

In Dendroscope, a rooted phylogenetic network is described as a single line of extended-Newick format using brackets, as in the description of a rooted phylogenetic tree in the standard Newick format, with additional labels placed at the end of node labels. These special labels are of the form '#H1', '#H2', etc. When parsing an extended-Newick string, all nodes whose labels end on '#H1' are identified with each other, all nodes that end on '#H2' are identified, etc.

For example, to describe a rooted phylogenetic network with three leaves labeled 'a', 'b' and 'c', in which 'b' is to have a "reticulate" parent node that connects both above 'a' and above 'c', use the following extended-Newick string:

```
((a,(b)#H1),(c,#H1));
```

Copy and paste this string into a Dendroscope window to see the corresponding network.

In Dendroscope, anything that can be done with a rooted tree can also be done with a rooted phylogenetic network!

8.5 Graphics Formats

The following `graphics formats` are supported (how to open the `Export Image` dialog see 6.4):

- JPEG, “Joint Photographic Experts Group”.
- GIF, “Graphics Interchange Format”.
- EPS, “Encapsulated PostScript”.
- SVG, “Scalable Vector Graphics”.
- PNG, “Portable Network Graphics”.
- BMP, “Bitmap”.
- PDF, “Portable Document Format”.

9 Commands

The program provides a command-intepreter to access all its functionalities. a *command* can be entered either using the `Window→Enter Command` item or by starting the program in command-line mode and typing (or piping) commands to the program via the console.

The `Command` window has a field for entering commands, a cancel button and two two different apply buttons. The Apply button applies the entered command to the current tree, whereas the Apply to All button applies the entered command to all trees in the current file.

Here is a summary of all available commands:

```
Opening and saving files:
        open file=name [init=command] - Open the named file in the current window, if empty, otherwise in a new window,
                                        and then optionally perform specified initial commands in new window
        launch file=name -              Open the named file in the current window
        save [format=value] file=name - Save data to file in the specified format (possible formats: nexus newick dendro)
        exportgraphics [format={EPS|PNG|GIF|JPG|SVG|PDF}] [replace=bool] [textasshapes=bool] [title=title] file=filename -
                                        Export a picture of the current tree
        source file=name -              Read commands from the named file

Choosing tree and visualization:
        set which=value -               Sets the current tree (possible values: number-of-tree first last previous next)
        set drawer=drawer-name -        Set the drawer used to draw the tree
                                        (Possible values: RectangularPhylogram RectangularCladogram SlantedCladogram
                                        RadialPhylogram RadialCladogram CircularPhylogram CircularCladogram InnerCircularCladogram)
        set auxilaryparameter=number -  Set the auxilary parameter used by some of the drawers

Customizing the layout of a tree:
        reroot -                        Reroot current tree using currently selected set of nodes (outgroups), node or edge
        ladderize=value -               Ladderize each displayed tree (possible values: left right random none)
        rotatesubtree -                 Rotate all children of all selected nodes
        swapsubtree -                   Swap subtree below selected node(s)
        reset labelpositions -          Reset all node label positions
        center -                        Center the tree
        rotate angle=number -           Rotate the whole tree by the given angle (in radian)
        set hflip=bool -                Flip the tree horizontally?
        rotatelabels -                  Rotate the labels of selected nodes

Adding, creating and modifying trees:
        add tree=newick-tree -          Add the specified tree to the list of trees
        duplicate -                     Duplicate the current window
        extractsubtree -                Extract the subtree induced by the currently selected nodes
        extractlsatree -                Extract the LSA-tree from a rooted network
        remove taxa={selected| names} - Remove all selected taxa, if taxa=selected, otherwise, remove named taxa
        compute consensus=value         Compute a consensus tree or network of a set of trees
                                        (possible values: Strict Majority Loose Network LSA)
        remove innerlabels -            Remove all labels of inner nodes
        apply command -                 Applies the given command to all trees in the file

Selection and Deselection:
        select all -                    Select all nodes and edges
        select nodes -                  Select all nodes
```

```
        select edges -                  Select all edges
        select previous -               Select all labeled nodes as in previous window
        select labelednodes -           Select all labeled nodes
        select leaves -                 Select all leaves
        select subtree -                Select all nodes in subtrees below selected
        select subpart -                Select part of subtree
        select nonterminal -            Select all non-terminal nodes
        select intermediate -           Select all intermediate nodes
        select root -                   Select root
        select special -                Select all 'special' edges
        select invert -                 Invert the current selection
        deselect all -                  Deselect all nodes and edges
        deselect nodes -                Deselect all nodes
        deselect edges -                Deselect all edges
        list taxa=selected -            List all currently selected taxa

Searching:
        find searchtext=text target={Nodes|Edges} [all=bool] [regex=bool] [wholeword=bool] [respectcase=bool] -
                                                Find and select the next label matching the given search text
        replace searchtext=text replacetext=text [target={Nodes|Edges}] [all=bool]
                                                        [regex=bool] [wholeword=bool] [respectcase=bool] -                                                                                                Find an

Collapsing and uncollapsing nodes:
        collapse all -                  Collapse all nodes
        collapse selection -            Collapse all selected nodes
        collapse complement -           Collapse the complement of all selected nodes
        collapse level=number -         Collapse all nodes at the given level (distance from root)
        uncollapse all -                Uncollapse  all nodes
        uncollapse selection -          Uncollapse all selected nodes
        uncollapse subtree -            Uncollapse whole subtree for selected nodes

Visualization:
        set window [width=num] [height=num] [x=num] [y=num]-
                                        Set size and location of main window
        set font=name                   Set font by name
        set autolayoutlabels=bool -     Set auto-layout of labels
        set margin [left=num] [right=num] [top=num] [bottom=num] -
                                        Set the margin around the tree
        show approxthreshold=int -      Set minimum threshold for representing subtrees by approximate shapes
        show edgelabels=bool -          Show or hide edge lbels
        show edgeweights=bool -         Show or hide edge weights
        show nodelabels=bool -          Show or hide node labels
        show intermediatenodelabels=bool -
                                        Show or hide labels of intermediate nodes
        set maintainedgelengths=bool -  When set, edge lengths cannot be changed, when not set, edges can be stretched
        set eshape=value -              Set the shape of selected edges (possible values: polygon quadratic cubic)
        set nshape=value -              Set the shape of selected nodes (possible values: rect oval)
        set radiallabels=bool -         Set radial layout of node labels
        set sparselabels=bool -         Set sparse layout of node labels (in which labels that would overlap others are not shown)
        set color=color -               Set the color of all selected nodes and edges
        set bgcolor=color -             Set the background color of all selected nodes
        set labelcolor=color -          Set the label color of all selected nodes and edges
        set edgewidth=number -          Set the line width of all selected edges
        set nodesize=number -           Set the size of all selected edges

Scaling:
        contract direction=horizontal - Contract tree horizontally
        contract direction=vertical -   Contract tree vertically
        expand direction=horizontal -   Expand tree horizontally
        expand direction=vertical -     Expand tree vertically
        zoom selection -                Zoom to current selection of nodes
        zoom fit -                      Zoom to fit whole tree in window
        reset view -                    Reset the scaling of the tree

Controlling the magnifier:
        set magnifier=bool -            Turn magnifier on or off
        set magradius=number -          Set magnifier radius
        set magdisplacement=number -    Set magnifier displacement (power)
        set magnifyallmode=bool         Set the magnifier all mode

Adding images to nodes:
        load imagedir=directory-name -Load image files from named directory. Images are placed next to taxa of same name
        set imageheight=num -           Set the height of the images associated with all selected nodes
        set imagelayout=value -         Set the layout used for images (possible values: north south east west radial)

Special purpose:
        update -                        Update the computation
        metasim -                       Run metasim commands
        set dirty=bool -                Set the dirty status of a document
        set vint=bool -                 Set show version-in-window-title mode
        set scalebar=bool -             Set show scalebar mode
        setprop name=boolean -          Set the boolean value of a named property

Other:
        version -                       List version info
        help -                          List this help
        about -                         List information about Dendroscope
        quit -
```

10 Examples

Figures 1 through 3 illustrate the major views possible with Dendroscope , as well as the action of the Magnifier and the editing possibilities.

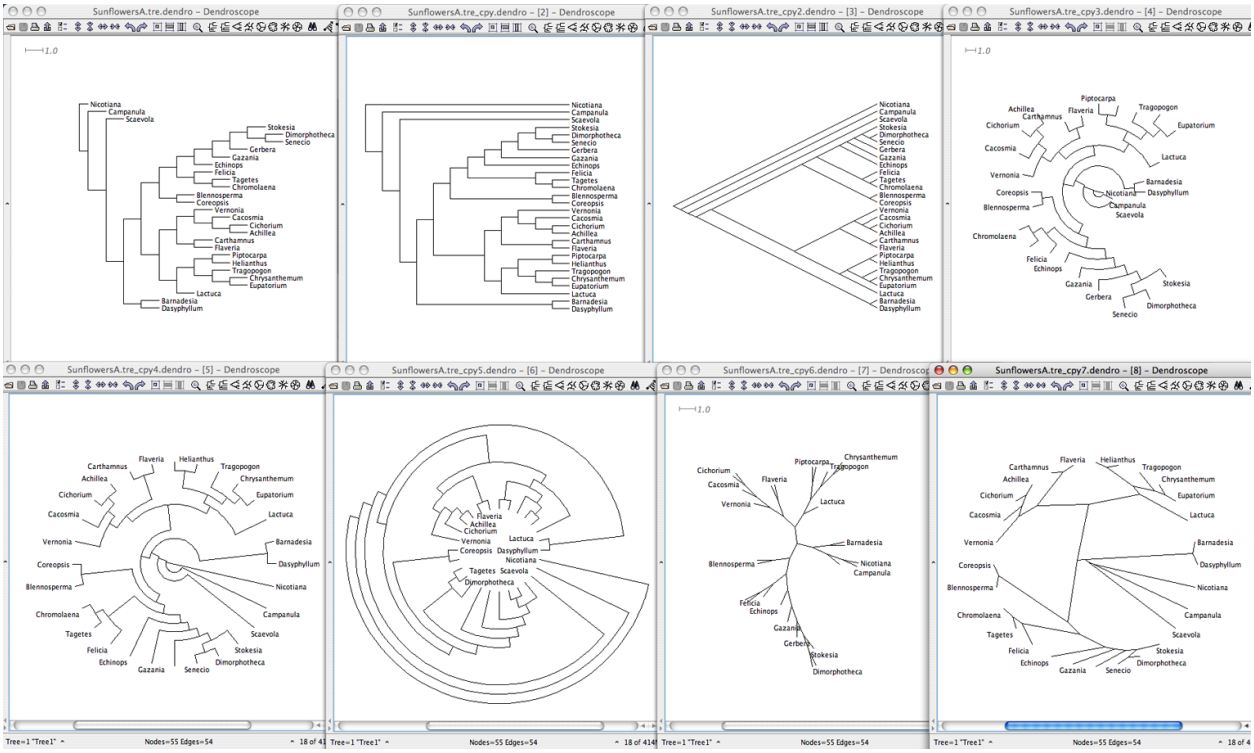

Figure 1: Illustration of the eight views possible with Dendroscope . Upper line: Rectangular Phylogram, Rectangular Cladogram, Slanted Cladogram, Circular Phylogram. Lower line: Circular Cladogram, Internal Circular Cladogram, Radial Phylogram, Radial Cladogram.

11 Acknowledgements

This program includes software developed by the Apache Software Foundation (http://www.apache.org/), namely the *Batik* library for generating image files. It also uses *MRJAdapter* , a Java package used to help construct user interfaces for the Apple Macintosh. This program uses Daniel Huson's unpublished `jloda` library, which is also used by SplitsTree4 (http://www.splitstree.org)[2].

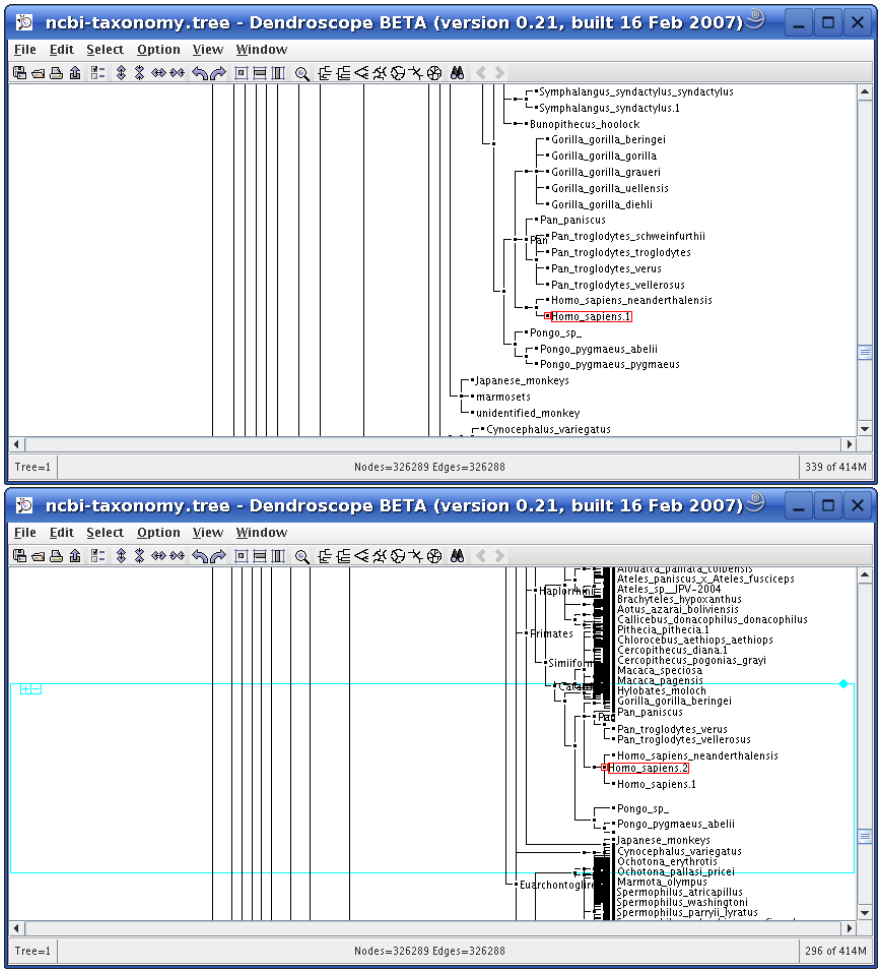

Figure 2: Part of the NCBI taxonomy showing *Homo sapiens* and his relatives without and with the magnifier turned on.

References

[1] Gabriel Cardona, Francesc Rossell, and Gabriel Valiente. Extended newick: It is time for a standard representation, 2008. Submitted to BMCB, http://bioinfo.uib.es/media/uploaded/bmc-2008-enewick-sub.pdf.

[2] Daniel H. Huson. Splitstree: analyzing and visualizing evolutionary data. *BIO*, 14(1):68–73, 1998. http://bioweb.pasteur.fr/docs/doc-gensoft/splitstree/splitstree.ps.

[3] Daniel H. Huson. Drawing rooted phylogenetic networks. *TCBB*, 2008. To appear.

[4] Daniel H. Huson, Tobias Dezulian, Markus Franz, Christian Rausch, Daniel C. Richter, and Regula Rupp. Dendroscope - an interactive tree drawer. *BMCB*, 8:460, 2007. http://dx.doi.org/10.1186/1471-2105-8-460, software freely available from http://www-ab.informatik.uni-tuebingen.de/software/dendroscope/.

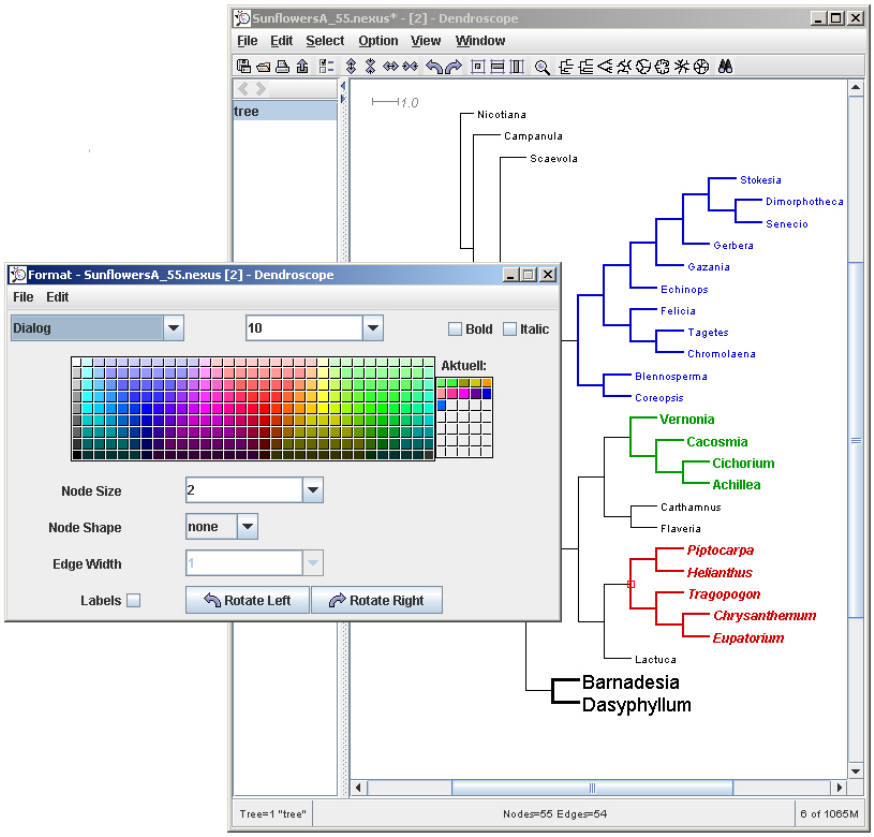

Figure 3: All labels and tree substructures can be easily edited.

[5] Daniel H. Huson, Regula Rupp, Vincent Berry, Gambette Philippe, and Christophe Paul. To appear in: RECOMB, 2009.

[6] Regula Rupp and Daniel H. Huson. Summarizing multiple gene trees using cluster networks. In *WABI08*, 2008.

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